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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 9, 2002, 04:35:07 ; Search time 2784 Seconds

(without alignments)
1986.183 Million cell updates/sec

Title: US-09-895-298A-83
Perfect score: 1002
Sequence: 1 MMNFQPPSKAMRASQMMTF.....HDGSLDLRSRSVQEGNPRA 190

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=numan4.0.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	100.0	1219	6 AX108540	AX108540 Sequence
2	1002	100.0	1813	9 AK023655	AK023655 Homo sapi
3	1002	100.0	1960	6 AX108538	AX108538 Sequence
4	1002	100.0	2407	6 AX108534	AX108534 Sequence
5	1002	100.0	2521	6 AX108536	AX108536 Sequence
6	1002	100.0	2760	9 BC027602	BC027602 Homo sapi
7	995	99.3	2387	9 AK093944	AK093944 Homo sapi
8	680	67.9	2399	9 AK097718	AK097718 Homo sapi
9	327	32.6	220633	9 HU091321	U91321 Human Chrom
10	327	32.6	223280	2 AC130456	AC130456 Homo sapi
11	307	30.6	71596	2 AC100877	AC100877 Mus muscu
12	293	29.2	1639	9 AB002405	AB002405 Homo sapi
13	293	29.2	1804	9 BC018346	BC018346 Homo sapi
14	293	29.2	5291	9 AK074065	AK074065 Homo sapi
15	291.5	29.1	2848	10 BC004840	BC004840 Mus muscu
16	290.5	29.0	1658	10 BC013502	BC013502 Mus muscu
17	253.5	25.3	1983	10 BC005510	BC005510 Mus muscu
18	253.5	25.3	2614	10 BC006956	BC006956 Mus muscu
19	228.5	22.8	81704	9 AL512353	AL512353 Human DNA
20	228.5	22.8	192180	2 AC023331	AC023331 Homo sapi
21	226.5	22.6	110000	2 AC124444_2	Continuation (3 of
22	212	21.2	402	6 AX071021	AX071021 Sequence
23	195.5	19.5	164564	9 HUAC003108	AC003108 Human Chr
24	184	18.4	623	10 MM0297000	AJ297000 Mus muscu
25	165.5	16.5	37026	9 CNS00YVF	AL096808 Homo sapi
26	165.5	16.5	177738	9 AC021593	AC021593 Homo sapi
27	158	15.8	193465	2 AL645856	AL645856 Mus muscu
28	118	11.8	2779	9 AK024893	AK024893 Homo sapi
29	107.5	10.7	1633	6 AX464084	AX464084 Sequence
30	105.5	10.5	168582	2 AC079534	AC079534 Mus muscu
31	104.5	10.4	1803	9 BC016931	BC016931 Homo sapi
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35	103	10.3	94212	2 AC091848	AC091848 Homo sapi
36	103	10.3	210202	2 AC008778	AC008778 Homo sapi
37	103	10.3	221452	9 AC034242	AC034242 Homo sapi
38	102.5	10.2	201309	10 AL669857	AL669857 Mouse DNA
39	101.5	10.1	185290	2 AL844560	AL844560 Mus muscu
40	101	10.1	162004	2 AC110554	AC110554 Mus muscu
41	101	10.1	171394	2 AC102779	AC102779 Mus muscu
42	101	10.1	194374	9 AC016766	AC016766 Homo sapi
43	100	10.0	71596	2 AC100877	AC100877 Mus muscu
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RESULT 1

ALIGNMENTS

AXI08540
 LOCUS AXI08540 1219 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 7 from Patent WO0123417.
 ACCESSION AXI08540
 VERSION AXI08540.1 GI:13923839
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS 1 (bases 1 to 1219)
 TITLE vinals y de Bassols,C.
 HUMAN tumor-associated lak-4p related polynucleotides and
 polypeptides and their uses
 PATENT: WO 0123417-A 7 05-APR-2001;
 JOURNAL SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
 FEATURES
 source 1. 1219
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 346 a 260 c 275 g 338 t
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 Pred. No.: 2,29e-102 Length: 1219
 Score: 1002.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-895-298A-83 (1-190) x AXI08540 (1-1219)

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 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
 Db 64 ATCTTCTGCTCTTTTCCATCTTTCACCGGGGCTGTGGACACCTGGCCATCACCATC 123
 QY 41 TPpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 Db 124 TGGAGATGAGAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGCTCTGCTTCATTCAC 183
 QY 61 SerIleTyrSerTTPileaspThrLeuSerThrArgProGlyTyrLeuTyrValValTrrp 80
 Db 184 TCCATCTACAGCTGATCGACACCCCTAAGTACACGGCGCTGCTGCTGCTGCTGCTG 243
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
 Db 244 ATCTATGGGAACCTCATTTGGAAGTGTGCACTTTTTCATCTTCACCCCTCATTTGCTG 303
 QY 101 IleIleThrTyrLeuTyrTrrpGlnIleThrGlyGlyArgLysIleMetIleArgLeuLeu 120
 Db 304 ATCATCACCTATCTTACTGCGACATCACAGAGGAGAGATATGATTAAGGCTGCTC 363
 QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
 Db 364 CATGAGCAGATCATTAATGAGGGCAAGATAAATGTCTGATAGAAAAATTGATCAAG 423
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGluVal 160
 Db 424 CTGACAGATATGAGGAAGAAAGCAAAACCCACCTCCTGTTCTGGAAAGAGAGAGGCTG 483
 QY 161 GlnGlnGlnGlyPheLeuHisLeuGlyGlnHisAspGlySerLeuAspLeuArgSerArg 180
 Db 484 GAGCAACAAGGCTTTTTCATTTGGGGGAGACATGATGAGCAGTCTTGACTTGCATCAGA 543
 QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
 Db 544 AGATCAGTTCAAGAAAGTAAATCCAAAGGCC 573

RESULT 2
 LOCUS AK023655 1813 bp mRNA linear PRI 01-AUG-2002
 DEFINITION Homo sapiens CDNA FLJ13593 fls, clone PLACE1009493.
 ACCESSION AK023655
 VERSION AK023655.1 GI:10435644
 KEYWORDS oligo capping; fls (full insert sequence).
 SOURCE Homo sapiens placenta CDNA to mRNA, clone_1lb:PLACE1
 clone:PLACE1009493.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 AUTHORS 1
 TITLE Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoi,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
 Nakamura,Y., Nagahari,K., Masuno,Y., Ninomiya,K. and Iwayanagi,T.
 NEDO human CDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1813)
 AUTHORS Isogai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human CDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; CDNA full insert
 sequencing: Research Association for Biotechnology; CDNA library
 construction, 5' - 6 3' -end one pass sequencing and clone selection;
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.

COMMENT

FEATURES
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 1. 1813
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 /db_xref="taxon:9606"
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 31. 1023
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CDS

BASE COUNT 489 a 400 c 405 g 519 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.78e-102 Length: 1813
 Score: 1002.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-895-298A-83 (1-190) x AK023655 (1-1813)

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 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40

Db 511 ATCTTCTGCTCTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCCTGGCCATCACCATC 570
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 571 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCCTCTTCATTCAC 630
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTyr 80
Db 631 TCCATCTACAGCTGGATGCACACCCCTAAGTACACGGCCTGGCTACCTGTGGTTGGTGG 690
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 691 ATCTATCGGAACCTCATTTGGAAGTGTGCACATCTTTTCATCCTCACCCCTCATTTGGCTA 750
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyValArgLysIleMetIleArgLeu 120
Db 751 ATCATCACTATCTTTACTGGCAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 810
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
Db 811 CATGACAGATCATTTAATGAGGCAAGATAAATGTTCTGTAGAAATAATTGATCAAG 870
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGluVal 160
Db 871 CTGACGATATGAGAAAGCAAAACCCGACTGTTGTTCTGAAAGAGAGAGGTG 930
QY 161 GluGlnGlnGlyPheLeuHisLeuGlnGlyLysAspGlySerLeuAspLeuArgSerArg 180
Db 931 GAGCAACAAGCCTTTTGTGATTTGGGGGACATGATGCGACTTGTGACTTGGCATCTAGA 990
QY 181 ArgSerValGlnGlnGlyLysProArgAla 190
Db 991 AGATCAGTTCAAGAGGTAAATCCAAAGGCC 1020

RESULT 3

AX108538 1960 bp DNA linear PAT 30-APR-2001
LOCUS AX108538
DEFINITION Sequence 5 from Patent WO0123417.
ACCESSION AX108538
VERSION AX108538.1 GI:13923838
KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
HUMAN tumor-associated lak-4p related polynucleotides and
polypeptides and their uses

JOURNAL

Patent: WO 0123417-A 5 05-APR-2001;

SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES

source

1.1960
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 515 a 439 c 447 g 559 t

ORIGIN

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Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-895-298a-83 (1-190) x AX108538 (1-1960)

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QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40

Db 805 ATCTTCTGCTCTTTTCCCATCTTTCACCGGGGTCTTGTGCACCCCTGGCCATCACCATC 864
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 865 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCCTCTTCATTCAC 924
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTyr 80
Db 925 TCCATCTACAGCTGGATGCACACCCCTAAGTACACGGCCTGGCTACCTGTGGTTGGTGG 984
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
Db 985 ATCTATCGGAACCTCATTTGGAAGTGTGCACATCTTTTTCATCTCACCCCTCATTTGCTG 1044
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyValArgLysIleMetIleArgLeu 120
Db 1045 ATCATCACTATCTTTACTGGCAGATCACAGAGGAGGAAGATTATGATTAAGGCTGCTC 1104
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Db 1105 CATGACAGATCATTTAATGAGGCAAGATAAATGTTCTGTAGAAATAATTGATCAAG 1164
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGluVal 160
Db 1165 CTGACGATATGAGAAAGCAAAACCCGACTGTTGTTCTGAAAGAGAGAGAGGTG 1224
QY 161 GluGlnGlnGlyPheLeuHisLeuGlnGlyLysAspGlySerLeuAspLeuArgSerArg 180
Db 1225 GAGCAACAAGCCTTTTGTGATTTGGGGGACATGATGCGACTTGTGACTTGGCATCTAGA 1284
QY 181 ArgSerValGlnGlnGlyLysProArgAla 190
Db 1285 AGATCAGTTCAAGAGGTAAATCCAAAGGCC 1314

RESULT 4

AX108534 2407 bp DNA linear PAT 30-APR-2001
LOCUS AX108534
DEFINITION Sequence 1 from Patent WO0123417.
ACCESSION AX108534
VERSION AX108534.1 GI:13923834
KEYWORDS

SOURCE

human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
HUMAN tumor-associated lak-4p related polynucleotides and
polypeptides and their uses

Patent: WO 0123417-A 1 05-APR-2001;

SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)

FEATURES

source

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/db_xref="taxon:9606"

BASE COUNT 635 a 557 c 546 g 669 t

ORIGIN

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Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-895-298a-83 (1-190) x AX108534 (1-2407)

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Db 1252 ATCTTCTGCTCTTTTCCCACTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC 1311
QY 41 TTPARGLEULYSPROSERAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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Db 1312 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCCTGCTCTTCATTAC 1371
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
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QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValleu 100
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1492 ATCATCACCCTATCTTACTGTGCAGATCACAGAGGGAAGATATGATAGGCTGCTC 1551
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1552 CATGAGCAGATCATTAATGAGGGCAAGATAAATGTTCTCGATAGAAAAATTGATCAAG 1611
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160
1612 CTGCAGATATGAGAGAAGCAACCCAGCTCCTTCTGTGAAAGAGAGAGGTG 1671
QY 161 GlnGlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
1672 GAGCAACAGAGCTTTTGGCATTTGGGGGAACATGATGGCAGTCTTGATGATCTAGA 1731
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QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
1732 AGATCAGTCAAGAGGTATCCCAAGGGCC 1761

RESULT 5
AX108536

LOCUS AX108536 2521 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 3 from Patent WO0123417.
ACCESSION AX108536
VERSION AX108536.1 GI:13923835

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 2521)
HUMAN tumor-associated lak-4p related polynucleotides and

JOURNAL
SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
location/Qualifiers
1. 2521

BASE COUNT 662 a 583 c 583 g 693 t
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/db_xref="taxon:9606"

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Pred. No.: 5.74e-102 Length: 2521
Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-895-298A-83 (1-190) x AX108536 (1-2521)

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Db 1366 ATCTTCTGCTCTTTTCCCACTTCACCGGGGCTTGTGCACCCCTGGCCATCACCATC 1425
QY 41 TTPARGLEULYSPROSERAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
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QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValIleTrp 80
1486 TTCATCTACAGCTGTGATCGACACCCCTAAGTACAGGCGCTGCTACCTGTGGTGTGG 1545
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValleu 100
1546 ATCTATCGGAACCTCATTTGGAAGTGTGCACCTTTTTCATCTCCTCACCTCATTTGTGCTA 1605
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgGlyIleMetIleArgLeuLeu 120
1606 ATCATCACCCTATCTTACTGTGCAGATCACAGAGGGAAGATATGATAGGCTGCTC 1665
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIleLys 140
1666 CATGAGCAGATCATTAATGAGGGCAAGATAAATGTTCTCGATAGAAAAATTGATCAAG 1725
QY 141 LeuGlnAspMetGlnLysLysAlaAsnProSerSerLeuValLeuGlnArgGlnVal 160
1726 CTGCAGATATGAGAGAAGCAACCCAGCTCCTTCTGTGAAAGAGAGAGGTG 1785
QY 161 GlnGlnGlnGlyPheLeuHisLeuGlnHisAspGlySerLeuAspLeuArgSerArg 180
1786 GAGCAACAGAGCTTTTGGCATTTGGGGGAACATGATGGCAGTCTTGATGATCTAGA 1845
Db 1786 GAGCAACAGAGCTTTTGGCATTTGGGGGAACATGATGGCAGTCTTGATGATCTAGA 1845
QY 181 ArgSerValGlnGlnGlyAsnProArgAla 190
1846 AGATCAGTCAAGAGGTATCCCAAGGGCC 1875

RESULT 6
BC027602

LOCUS BC027602 2760 bp mRNA linear PRI 01-MAY-2002
DEFINITION Homo sapiens, Similar to RIKEN cDNA 4932443L08 gene, clone
MGC:26648 IMAGE:4839111, mRNA, complete cds.

ACCESSION BC027602
VERSION BC027602.1 GI:20381190
KEYWORDS MGC.

SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 2760)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL
Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shlrahi
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadanesystemsbiology.org
Anup Madan, Jessica Fahy, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 34 Row: p Column: 13
This clone was selected for full length sequencing because it

passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein.

FEATURES

source

1..2760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/tissue_type="Testis"
/clone_1lb="NH.MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"
213..2495
CDS
/codon_start=1
/product="Similar to RIKEN cDNA 4932443L08 gene"
/protein_id="AAH27602.1"
/db_xref="GI:20381191"
/translation="MISDDHNEITIOVENSSGVQSHSSNQIFQEKVLDDSSINW
LSISDIDVIDSQTSKRNDQKNOVLRRSTLSMESQTLHSLCEMGIDTPSSHETV
OGOKLIASLIPMTSRDRIKAIKRNQPRIMEEKRNLKIVDEKSKQTHRILOKNCIOC
LNSISRAVRSKNSLSEILNISLSLWQTKIIGKFGTSVLSYFNFLRWLLEFNISF
ILNFSFIIPQFTYAKKNTLQFTGLFEFTGVYERDVTMYGFTYSTIOHNSGASY
NMOLAYITIGACLTTCFSLFSMAKFRNNFINPHYSGGITKLIFCWDFTVTHEK
AVRLKQNSTEIRNLSLROENSKLLENOILRFSAVAVAVAVSVAIAACAAV
VLAEVNLEFKTHSNPQVILLPEVNSCINLAVPCISMPRLVEREPRHVEYVILL
RNIFLKISITIGILCYWLNVAALSGEECWETLIGODIYRLLMDENFSLVNSFLGEPL
RRIIGMOLITSLIOEDIANVLELIYAQTLWIGIFCPDLPFIOMIMLFIMFYSK
NISLMNRPQPSKAMRASQMMTFILFFPSFTGVLCITAITWRLKPSADCGPFRG
LPLFIHSIYSWIDLTSTPGYLWVWVYIRNLIGSVHFFELITLIVLITLYWQITEG
RKIMIRLHEQIINGCKDKMFLIEKLKIQDMERKANPSLVLERREVEQGFHLHGE
HDSGLDRSRRSVQEGNPRA"

BASE COUNT 739 a 637 c 625 g 759 t
ORIGIN

Alignment Scores:

Pred. No.: 6.44e-102 Length: 2760
Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-895-298a-83 (1-190) x BC027602 (1-2760)

QY 1 MetMetasnpheglnProProserLysalaTprArgAlaSerGlnMetMethrphphe 20
|||||
Db 1923 ATGATGAATTCAGACCTCGAGCAAGCCTGGCGGCTCAGAGATGATGATCTTCTC 1982
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuGlyThrLeuAlaIleThrIle 40
|||||
Db 1983 ATCTTCTTGCTCTTTTCCATCCTTCACCGGGGCTGTGTGCACCTGGCCATCACCATC 2042
QY 41 TTPArgLeuLysProSerAlaAspGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
Db 2043 TGGAGATGGAAGCCTTCAGCGACTGTGGCCCTTTTCGAGGTCTGCCTCTTCATTTCAC 2102
QY 61 SerIleYrSerTrpIleAspThrIleSerThrArgProGlyTrpValLeuValTrp 80
|||||
Db 2103 TCCATCTACAGCTGAGTGCAGACCTTAAGTACAGCGCTGGCTACCTGTGGGTGTGG 2162
QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleValLeu 100
|||||
Db 2163 ATCTATCGGAACCTCATTTGAGAGTGTGCACCTCTTTTCATCCTCACCCTCATTTGTGCTA 2222
QY 101 IleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyIleMetIleArgLeuLeu 120
|||||
Db 2223 ATCATCACCTATCTTACTGCGAGATCACAGAGGAAGAAAGATATGATAGAGCTGCTC 2282
QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
|||||
Db 2283 CATGAGCAGATCATTAATGAGGGCAAAAGATAAATGTTCTGATAGAAAATTTGATCAAG 2342
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
|||||

Db 2343 CTGCAGATATGAGAGAAGAAAGCAACCCACCTCCTGTTCTTGCAAAAGAGAGGTG 2402

QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
|||||

Db 2403 GAGCAACAAAGGCTTTTTCGATTTGGGGGAACATGATGCAGTCTTGACCTTGCATCTAGA 2462

QY 181 ArgSerValGlnGlyLysProArgAla 190
|||||

Db 2463 AGATCAGTTCAAGAAAGTAAATCCAAAGGCC 2492

RESULT 7

AK093944

LOCUS

DEFINITION Homo sapiens cDNA FLJ36625 fis, clone TRACH2017368, weakly similar to Homo sapiens mRNA for LAK-4p.

ACCESSION

AK093944

VERSION

AK093944.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, R., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E., Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Irie, R., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and Isogai, T.

NEO human cDNA sequencing project

Unpublished

2 (bases 1 to 2387)

Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

FEATURES

source

1..2387
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TRACH2017368"
/tissue_type="trachea"
/clone_1lb="TRACH2"
/note="cloning vector: pME18SFL3"

BASE COUNT 624 a 549 c 543 g 671 t
ORIGIN

Alignment Scores:

Pred. No.: 3.24e-101 Length: 2387
Score: 995.00 Matches: 189
Percent Similarity: 99.47% Conservative: 0
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 99.30% Indels: 0
DB: 9 Gaps: 0

US-09-895-298a-83 (1-190) x AK093944 (1-2387)

QY 1 MetMetasnpheginProProserlysaLatrpArgAlaSerGlnMetMetThrPhephe 20
|||||
Db 1025 ATGATGAATTTCCAGCCTCCGAGCAAAAGCCCTGGCGGCTCGCAGATGATGACTTCTTC 1084
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
|||||
Db 1085 ATCTTCTTGCTCTTTTCCATCCTTACCGCGGGCTCTTGACACCCCTGGCCATCACCAATC 1144
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
Db 1145 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGCTGCTCTTCATTCAC 1204
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80
|||||
Db 1205 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCTGGCTACCTGTGGTGTGG 1264
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
|||||
Db 1265 ATCTATCGAACCCTCATTTGGAAGTGTGCTCTTTTCATCTCCTCACCCCTCATTTGTGCTA 1324
QY 101 IleIleThrTyLeuTyTrpGlnIleThrGlyArgLysIleMetIleArgLeuLeu 120
|||||
Db 1325 ATCATCACCTATCTTTACTGCGCAGATACACAGAGGAAGATTATGATAAGGCTGCTC 1384
QY 121 HisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
|||||
Db 1385 CATGAGCAGATCATTAATGAGGCAAAAGATAAATGTTCTGATAGGAAAATTGATCAG 1444
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGlnArgArgGluVal 160
|||||
Db 1445 CTGCAGATATGAGAAAGAAAGCAAAACCCAGCTCCTGTTGTGAAAAGAGAGAGGTG 1504
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyLysIleHisAspGlySerLeuAspLeuArgSerArg 180
|||||
Db 1505 GAGCAACAAGGCTTTTTCATTTGGGGGAACATGATGCGAGTCTTGACTTGCGATCTAGA 1564
QY 181 ArgSerValGlnGlyAsnProArgAla 190
|||||
Db 1565 AGATCAGTTCAAGAGGTAATCCAAAGGCC 1594
RESULT 8
AK097718
LOCUS AK097718 2399 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ40399 fis, clone TEST12037081, weakly similar
to Homo sapiens mRNA for LAK-4p.
ACCESSION AK097718
VERSION AK097718.1 GI:21757573
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens testis cDNA to mRNA, clone_lib:TEST12
clone:TEST12037081.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Magatsuna,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
Suzuki,Y., Sugano,S., Nagahara,K., Masuno,Y., Nagai,K. and
Isogai,T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2399)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan: cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
source
1. 2399
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/db_xref="taxon:9606"
/clone="TEST12037081"
/tissue_type="testis"
/clone_lib="TEST12"
/note="cloning vector: pME18SFL3"
BASE COUNT 610 a 591 c 528 g 670 t
ORIGIN
Alignment Scores:
Pred. No.: 5,14e-66 Length: 2399
Score: 680.00 Matches: 126
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.86% Indels: 0
Gaps: 0
US-09-895-298a-83 (1-190) x AK097718 (1-2399)
QY 1 MetMetasnpheginProProserlysaLatrpArgAlaSerGlnMetMetThrPhephe 20
|||||
Db 1933 ATGATGAATTTCCAGCCTCCGAGCAAAAGCCCTGGCGGCTCGCAGATGATGACTTCTTC 1992
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
|||||
Db 1993 ATCTTCTTGCTCTTTTCCATCCTTCACCGGGCTGTGTGACCCCTGGCCATCACCATC 2052
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
|||||
Db 2053 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCTCTTCATTCAC 2112
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyLeuTrpValValTrp 80
|||||
Db 2113 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCTGGCTACCTGTGGTGTGG 2172
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
|||||
Db 2173 ATCTATCGAACCCTCATTTGGAAGTGTGCACTTCTTTTCATCTCCTCACCCCTCATTTGTGCTA 2232
QY 101 IleIleThrTyLeuTyTrpGlnIleThrGlyArgLysIleMetIleArgLeuLeu 120
|||||
Db 2233 ATCATCACCTATCTTTACTGCGCAGATCACAGAGGAAGAAAGATTATGATAAGGCTGCTC 2292
QY 121 HisGlnGlnIleIleAsn 126
|||||
Db 2293 CATGAGCAGATCATTAAT 2310
RESULT 9
HUU91321
LOCUS HUU91321 220633 bp DNA linear PRI 10-JAN-2000
DEFINITION Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.
ACCESSION U91321
VERSION U91321.1 GI:2951946
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 220633)
AUTHORS Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,
Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,
Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S.,
Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.
TITLE Genome duplications and other features in 12 Mb of DNA sequence
from human chromosome 16p and 16q
JOURNAL Genomics 60 (3), 295-308 (1999)

MEDLINE 99425270
PUBMED 10493829
REFERENCE 2 (bases 1 to 220633)
AUTHORS Adams,M.D., Loftus,B.J., Phillips,C.A., Zhou,L., Brandon,R.,
Fuhmann,J., and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 220633)
AUTHORS Adams,M.D., Loftus,B.J., Zhou,L. and Labombard,M.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-1997)
4 (bases 1 to 220633)
REFERENCE 4 (bases 1 to 220633)
AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (19-AUG-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 5 (bases 1 to 220633)
AUTHORS Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J. and
Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-1997) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
REFERENCE 6 (bases 1 to 220633)
AUTHORS Adams,M.D.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Mar 11, 1998 this sequence version replaced gi:2335062.
BAC clone CIT987SK-3636 is located in band 16p13.1 of chromosome
16. Genes were identified by a combination of five methods:
XGRail (available by anonymous ftp from arthur.epm.ornl.gov),
GeneFinder (available by anonymous ftp from
collneu.washington.edu), GENSCAN (available using the e-mail server
at genscan.genomic.stanford.edu), searches of the EST database at
TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a
peptide database. Repeats were identified using RepeatMasker (Smit,
A.F.A. and Green, P. unpublished,
http://ftp.genome.washington.edu/rm/RepeatMasker.html).
Location/Qualifiers
1. 220633
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/map="16p13.1"
/clone="A-363E6"
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/gene="363E6.1"
complement(join(82033..82152,82283..82349,107848..108338))
/gene="363E6.1"
complement(join(82117..82152,82283..82349,107848..107915))
/gene="363E6.1"
/codon_start=1
/product="Unknown gene product"
/protein_id="AAC05439.1"
/db_xref="GI:2951947"
/translation="MPTRPQPVPVPRLTSSQERIRHWCTRRLLSPDAGLVILDFPASR
TIMAPSAWFLF"
gene complement(217478..219568)
/gene="363E6.2"
complement(join(217478..218093,219357..219568))
/gene="363E6.2"
complement(join(217946..218093,219357..219568))
/gene="363E6.2"
/codon_start=1
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/protein_id="AAC05440.1"
/db_xref="GI:2951948"
/translation="WRQTRDVITALTTRPWSLSHTGDKRPYDTFWKHFTFVMDIL
IDMSHNILWYLCGISAFIMQKDFVSPAYLKKSAKGIVGVGWTVNTFDEKSYESH
GSSYITDSVVEDCEPHF"
BASE COUNT 61048 a 48977 c 49108 g 61449 t 51 others

ORIGIN
Alignment Scores:
Pred. No.: 4.39e-24 Length: 220633
Score: 327.00 Matches: 60
Percent Similarity: 96.83% Conservative: 1
Best Local Similarity: 95.24% Mismatches: 2
Query Match: 32.63% Indels: 0
DB: 9 Gaps: 0
US-09-895-298a-83 (1-190) x HUU91321 (1-220633)
QY 42 ArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHisSer 61
|||||
Db 204866 AGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGCTGCTGCTTCATTCACCTCC 204925
QY 62 IletYrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrpIle 81
|||||
Db 204926 ATCTACAGCTGATCGACACCCCTTAAGTACACGCGCTGCTACCTGTGGGTGTTGGATC 204985
QY 82 TyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeuIle 101
|||||
Db 204986 TATCGAACCCTCATTTGGAAGTGTGCACCTTTTTCATCCCTCACCCCTCATTTGTGCTGTA 205045
QY 102 IleThrTyr 104
Db 205046 GTGTGGTAC 205054
RESULT 10
AC130456 223280 bp DNA linear HTG 10-AUG-2002
LOCUS Homo sapiens chromosome 16 clone CTA-363E6, WORKING DRAFT SEQUENCE,
DEFINITION 5 unordered pieces.
AC130456
VERSION AC130456.1 GI:222033229
KEYWORDS HTGS_PHASE1, HTGS_DRAFT, HTGS_ACTIVEIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 223280)
REFERENCE DOE Joint Genome Institute.
AUTHORS Sequencing of Human Chromosome 16
JOURNAL Unpublished
2 (bases 1 to 223280)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 2773242
Center clone name: CIT978SKA_363E6

Summary Statistics
Consensus quality: 221100 bases at least Q40
Consensus quality: 222027 bases at least Q30
Consensus quality: 222494 bases at least Q20
Estimated insert size: 220633; agarose-fp estimation
Estimated insert size: 222880; sum-of-contigs estimation
Quality coverage: 10.81 in Q20 bases; agarose-fp estimation
Quality coverage: 10.71 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

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* be preserved.
* 1 1261: contig of 1261 bp in length
* 1262 1361: gap of unknown length
* 1362 2690: contig of 1329 bp in length
* 2691 2790: gap of unknown length
* 2791 32134: contig of 29344 bp in length
* 32135 32234: gap of unknown length
* 32235 102578: contig of 70344 bp in length
* 102579 102678: gap of unknown length
* 102679 223280: contig of 120602 bp in length.
FEATURES
    source
        1..223280
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="16"
            /clone="CTA-36356"
            /clone_11d="Caltech human BAC library A"
BASE COUNT    61286 a 49953 c 49351 g 62289 t 401 others
ORIGIN
Alignment Scores:
Pred. No.:      4.46e-24      Length:      223280
Score:          327.00      Matches:      60
Percent Similarity: 96.83%      Conservative: 1
Best local Similarity: 95.24%      Mismatches: 2
Query Match:    32.63%      Indels:      0
DB:             2      Gaps:      0
US-09-895-298a-83 (1-190) x AC130456 (1-223280)
QY 42 ArgLeuLysProSerAlaAspCysGlyProPhaArgGlyLeuProLeuPheIleHisSer 61
Db 86822 AGATTGAAGCCTTCAGCTGACTGTGCGCCCTTTCGAGGCTCGCCCTCTTCAATCACTCC 86881
QY 62 IleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrIleTrpValValTrpIle 81
Db 86882 ATCTACACGCTGAGTGCACACCTTAAGTACACGCGCTGCTACCTGGTGTGTGATC 86941
QY 82 TyrArgAsnLeuIleGlySerValHisPhePheIleLeuTrpIleValIle 101
Db 86942 TATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATTCCTCACCTCATTTGTGTGA 87001
QY 102 IleThrTyr 104
Db 87002 GTGTGTGTAC 87010
RESULT 11
AC100877
LOCUS          AC100877 71596 bp DNA linear HTG 23-NOV-2001
DEFINITION    Mus musculus clone RP23-35B17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION     AC100877
VERSION       AC100877.1 GI:17059651
KEYWORDS      HTG; HTGS_PHASE0.
SOURCE        Mus musculus.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 71596)
AUTHORS       Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE         Mus musculus, clone RP23-35B17
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 71596)
AUTHORS       Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczkzy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C.,
```

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TITLE
JOURNAL
COMMENT
* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
723 822: contig of 722 bp in length
823 1526: contig of 704 bp in length
1527 1626: gap of 100 bp
1627 2336: contig of 710 bp in length
2337 2436: gap of 100 bp
2437 3156: contig of 720 bp in length
3157 3256: gap of 100 bp
3257 3984: contig of 728 bp in length
3985 4084: gap of 100 bp
4085 4811: contig of 727 bp in length
4812 4911: gap of 100 bp
4912 5638: contig of 727 bp in length
5639 5738: gap of 100 bp
5739 6477: contig of 739 bp in length
6478 6577: gap of 100 bp
6578 7305: contig of 728 bp in length
7306 7405: gap of 100 bp
7406 8107: contig of 702 bp in length
8108 8207: gap of 100 bp
8208 8950: contig of 743 bp in length
8951 9050: gap of 100 bp
9051 9743: contig of 693 bp in length
9744 9843: gap of 100 bp
9844 10583: contig of 740 bp in length
10584 10683: gap of 100 bp
10684 11405: contig of 722 bp in length
11406 11505: gap of 100 bp
11506 12336: contig of 731 bp in length
12337 12336: gap of 100 bp
12337 13069: contig of 733 bp in length
13070 13169: gap of 100 bp
13170 13851: contig of 682 bp in length
13852 13951: gap of 100 bp
13952 14685: contig of 734 bp in length
14686 14785: gap of 100 bp
McCarthy,M., McEwan,P., McKernan,K., MCPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetli,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13918
Center clone name: 35_B_17
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* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
723 822: contig of 722 bp in length
823 1526: contig of 704 bp in length
1527 1626: gap of 100 bp
1627 2336: contig of 710 bp in length
2337 2436: gap of 100 bp
2437 3156: contig of 720 bp in length
3157 3256: gap of 100 bp
3257 3984: contig of 728 bp in length
3985 4084: gap of 100 bp
4085 4811: contig of 727 bp in length
4812 4911: gap of 100 bp
4912 5638: contig of 727 bp in length
5639 5738: gap of 100 bp
5739 6477: contig of 739 bp in length
6478 6577: gap of 100 bp
6578 7305: contig of 728 bp in length
7306 7405: gap of 100 bp
7406 8107: contig of 702 bp in length
8108 8207: gap of 100 bp
8208 8950: contig of 743 bp in length
8951 9050: gap of 100 bp
9051 9743: contig of 693 bp in length
9744 9843: gap of 100 bp
9844 10583: contig of 740 bp in length
10584 10683: gap of 100 bp
10684 11405: contig of 722 bp in length
11406 11505: gap of 100 bp
11506 12336: contig of 731 bp in length
12337 12336: gap of 100 bp
12337 13069: contig of 733 bp in length
13070 13169: gap of 100 bp
13170 13851: contig of 682 bp in length
13852 13951: gap of 100 bp
13952 14685: contig of 734 bp in length
14686 14785: gap of 100 bp
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14786 15512: contig of 727 bp in length
* 15513 15612: gap of 100 bp
* 15613 16342: contig of 730 bp in length
* 16343 16442: gap of 100 bp
* 16443 17175: contig of 733 bp in length
* 17176 17275: gap of 100 bp
* 17276 17973: contig of 698 bp in length
* 17974 18073: gap of 100 bp
* 18074 18798: contig of 725 bp in length
* 18799 18898: gap of 100 bp
* 18899 19622: contig of 724 bp in length
* 19623 19722: gap of 100 bp
* 19723 20437: contig of 715 bp in length
* 20438 20537: gap of 100 bp
* 20538 21266: contig of 729 bp in length
* 21267 21366: gap of 100 bp
* 21367 22094: contig of 728 bp in length
* 22095 22194: gap of 100 bp
* 22195 22903: contig of 709 bp in length
* 22904 23003: gap of 100 bp
* 23004 23745: contig of 742 bp in length
* 23746 23845: gap of 100 bp
* 23846 24584: contig of 739 bp in length
* 24585 24684: gap of 100 bp
* 24685 25327: contig of 643 bp in length
* 25328 25427: gap of 100 bp
* 25428 26144: contig of 717 bp in length
* 26145 26244: gap of 100 bp
* 26245 26977: contig of 733 bp in length
* 26978 27077: gap of 100 bp
* 27078 27776: contig of 699 bp in length
* 27777 27876: gap of 100 bp
* 27877 28595: contig of 719 bp in length
* 28596 28695: gap of 100 bp
* 28696 29420: contig of 725 bp in length
* 29421 29520: gap of 100 bp
* 29521 30246: contig of 726 bp in length
* 30247 30346: gap of 100 bp
* 30347 31069: contig of 723 bp in length
* 31070 31169: gap of 100 bp
* 31170 31896: contig of 727 bp in length
* 31897 31996: gap of 100 bp
* 31997 32740: contig of 744 bp in length
* 32741 32840: gap of 100 bp
* 32841 33583: contig of 743 bp in length
* 33584 33683: gap of 100 bp
* 33684 34406: contig of 723 bp in length
* 34407 34506: gap of 100 bp
* 34507 35237: contig of 731 bp in length
* 35238 35337: gap of 100 bp
* 35338 36065: contig of 728 bp in length
* 36066 36165: gap of 100 bp
* 36166 36880: contig of 715 bp in length
* 36881 36980: gap of 100 bp
* 36981 37694: contig of 714 bp in length
* 37695 37794: gap of 100 bp
* 37795 38521: contig of 727 bp in length
* 38522 38621: gap of 100 bp
* 38622 39349: contig of 728 bp in length
* 39350 39449: gap of 100 bp
* 39450 40190: contig of 741 bp in length
* 40191 40290: gap of 100 bp
* 40291 41012: contig of 722 bp in length
* 41013 41112: gap of 100 bp
* 41113 41852: contig of 740 bp in length
* 41853 41952: gap of 100 bp
* 41953 42688: contig of 736 bp in length
* 42689 42788: gap of 100 bp
* 42789 43523: contig of 735 bp in length
* 43524 43623: gap of 100 bp
* 43624 44318: contig of 695 bp in length
* 44319 44418: gap of 100 bp
* 44419 45138: contig of 720 bp in length

45139 45238: gap of 100 bp
* 45239 45976: contig of 738 bp in length
* 45977 46076: gap of 100 bp
* 46077 46808: contig of 732 bp in length
* 46809 46908: gap of 100 bp
* 46909 47613: contig of 705 bp in length
* 47614 47713: gap of 100 bp
* 47714 48431: contig of 718 bp in length
* 48432 48531: gap of 100 bp
* 48532 49280: contig of 749 bp in length
* 49281 49380: gap of 100 bp
* 49381 50139: contig of 759 bp in length
* 50140 50239: gap of 100 bp
* 50240 50966: contig of 727 bp in length
* 50967 51066: gap of 100 bp
* 51067 51797: contig of 731 bp in length
* 51798 51897: gap of 100 bp
* 51898 52632: contig of 735 bp in length
* 52633 52732: gap of 100 bp
* 52733 53448: contig of 716 bp in length
* 53449 53548: gap of 100 bp
* 53549 54266: contig of 718 bp in length
* 54267 54366: gap of 100 bp
* 54367 55107: contig of 741 bp in length
* 55108 55207: gap of 100 bp
* 55208 55927: contig of 720 bp in length
* 55928 56027: gap of 100 bp
* 56028 56757: contig of 730 bp in length
* 56758 56857: gap of 100 bp

Alignment Scores:
Pred. No.: 1.81e-22 Length: 71596
Score: 307.00 Matches: 56
Percent Similarity: 92.42% Conservative: 5
Best Local Similarity: 84.85% Mismatches: 5
Query Match: 30.64% Indels: 0
DB: 2 Gaps: 0

US-09-895-298a-83 (1-190) x AC100877 (1-71596)

QY 40 ILETpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheHle 59
: : : : :
Db 48651 GTCTTCAGACTGAACCTCGGCTGACTGTGGCCGCTCCGAGGTCTGCTTCATC 48710

QY 60 HisSerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpVal 79
: : : : :
Db 48711 CAATCATCTACAGCTGAGATTGACACTGTGACCGCAGCGCTGACTGTGGCTGTC 48770

QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleVal 99
: : : : :
Db 48771 TGGATTACCAAGATCTCATTTGGAAGTGTGACTTCTTCTTCATCCTCACCCCTCATTTGTG 48830

QY 100 LeuIleIleThrTyrLeu 105
: : : : :
Db 48831 CTGTAAGTGGGGTTCCTC 48848

RESULT 12
AB002405
LOCUS AB002405 1639 bp mRNA linear PRI 02-MAR-2000
DEFINITION Homo sapiens mRNA for LAK-4p, complete cds.
ACCESSION AB002405
VERSION AB002405.2 GI:7209573
KEYWORDS LAK-4p.
SOURCE Homo sapiens male lymphoid.mLT expressing LAK cell cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1639)
AUTHORS Abe,Y. and Takeoka,Y.
TITLE LAK-4 clone from the membrane lymphotoxin expressing subtraction
library
JOURNAL Published Only in DataBase (1998)
REFERENCE 2 (bases 1 to 1639)

AUTHORS Abe, Y. and Takaoka, Y.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Yasuhito Abe, Ehime University School of Medicine, The Second Department of Surgery, Shigenobu, Onsen-gun, Ehime 791-02, Japan (E-mail: yasuhito@ehime-u.ac.jp, Tel:+81-89-964-5111, Fax:+81-89-960-5334)
 COMMENT On Mar 8, 2000 this sequence version replaced gi.2760120.
 Sequence updated (05-Jan-1998)
 Sequence updated (29-Feb-2000).
 FEATURES
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 1. 1639
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /sex="male"
 /cell_type="mLr expressing LAK cell"
 /tissue_type="lymphoid"
 53. 1387
 /note="Its enhancement of expression is related with T/LAK-cell-activation, unpublished data."
 /codon_start=1
 /product="LAK-4p"
 /protein_id="BAA24179.2"
 /db_xref="GI:7209574"
 /translation="MAHSFGESYRVGSGIHATVFCSDYKVTOKRASRLQDNIR
 TRKELIAEWQLRHSRVSVCGRQAVALGLVWLICLGTALGCAVAHVSEFMISQSP
 EAAGQAVLVLPVLVGLNLGAPYLCLRVLALEPHDSVLELYVALICRNLIKLAII
 GLICYHMLGRVGVLOGCWEDFVGOELRYFLVMDFVLMIDLTFEGELVWRITSEKIL
 KRRKRPEDIRANVLELYGOTLTWGLVFSPLIPAVQIKLLVYVYKTSILANCO
 APRPWLASHMSTVFLLCFPAFLGAVFLCYAVWQVKSSTCGPRTLDYEAQR
 VVVRHLEAGPRVSWLPVHRYLMENTFVFLVALLAVIYLNQVVRGQRVLCIL
 KEQISNEGEDKIFLNKLHSYERKERERSRVGTTEAAPALLTDEQDA"
 polyA_site
 1614
 BASE COUNT 294 a 495 c 517 g 333 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.55e-23 Length: 1639
 Score: 293.00 Matches: 63
 Percent Similarity: 53.76% Conservative: 37
 Best Local Similarity: 33.87% Mismatches: 66
 Query Match: 29.24% Indels: 20
 DB: Gaps: 3
 US-09-895-298A-83 (1-190) x AB002405 (1-1639)
 QY 1 MetMetAsnPhenGlnProProSerLysAlaTrpArgAlaSerGlnMetMetPhenPhe 20
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 866 CTGGCCACTGCGACGGCGCGCGCGCGCGCTGGCTGCCTACACATGAGCACCCTCTTC 925
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuLeuLeuLeuAlaIleThrIle 40
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 926 CTCACGCTGCTC 985
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 986 TGGCAGTGAAGCCCTCGACACCTGGGGCCCTCCGACACCTGACACCATGATGACAG 1045
 QY 61 SerIleTyrSerTrpIleAspThrLeu--SerThrArgProGlyTyrLeuTrpValVal 79
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 1046 GCCGGCAGAGGTGTGGCGCCACCGACGCGGCGGCGGCGGCTCTCTCTCTCTCTCTC 1105
 QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleVal 99
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 1106 TGGGTGACACCGGTACCTGATGGAACACCTCTTCTTCTCTCTCTCTCTCTCTCTCTG 1165
 QY 100 LeuIleIleThrTyrLeuTyrTrpGlnIleThrGlnGlyArgLysIleMetIleArgLeu 119
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 1166 CTGGCCGTGATCTACCTCAACATCCAGGTGTGGCGGCGGCGGCGGCAAGGTATCTGCTG 1225
 QY 120 LeuHisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIle 139
 :::: |||| |||| |||| :::: |||| |||| |||| |||| |||| ||||
 Db 1226 CTCAGGAGCAGATCAGCATGAGGTGAGGACAAATCTTCTTAATCAACAAGCTTCAC 1285

QY 140 LysLeuGlnAsp-----MetGlnLysLys 147
 :::: :::: |||| ::::
 Db 1286 TCCATCTACGAGCT 1345
 QY 148 AlaAsnProSerSerLeuValLeuGlnArgArgGlnValGlnGlnGlnGlnPheLeuHis 167
 |||| |||| :::: |||| :::: :::: ::::
 Db 1346 GCGGCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1384
 QY 168 LeuGlyGlnHisAspGly 173
 |||| :::: ||||
 Db 1385 TAGGGGAGCGCGATGGG 1402
 RESULT 13
 BC018346
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Homo sapiens.
 Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 1 (bases 1 to 1804)
 Strausberg, R.
 Direct Submission
 Submitted (03-DEC-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: villalobcm.tmc.edu.
 Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Series: IRAC Plate: 21 Row: 9 Column: 17
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 7305226.
 FEATURES
 source
 1. 1804
 /organism="Homo sapiens"
 /db_xref="LocusID:11322"
 /db_xref="taxon:9606"
 /clone="MGC:8770 IMAGE:3862414"
 /tissue_type="Ovary, adenocarcinoma"
 /clone_lib="NIH_MGC_66"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 209. 1543
 /codon_start=1
 /product="expressed in activated T/LAK lymphocytes"
 /protein_id="AAH18346.1"
 /db_xref="GI:17390810"
 /translation="MAHSFGESYRVGSGIHATVFCSDYKVTOKRASRLQDNIR
 TRKELIAEWQLRHSRVSVCGRQAVALGLVWLICLGTALGCAVAHVSEFMISQSP
 EAAGQAVLVLPVLVGLNLGAPYLCLRVLALEPHDSVLELYVALICRNLIKLAII
 GLICYHMLGRVGVLOGCWEDFVGOELRYFLVMDFVLMIDLTFEGELVWRITSEKIL
 KRRKRPEDIRANVLELYGOTLTWGLVFSPLIPAVQIKLLVYVYKTSILANCO
 APRPWLASHMSTVFLLCFPAFLGAVFLCYAVWQVKSSTCGPRTLDYEAQR
 VVVRHLEAGPRVSWLPVHRYLMENTFVFLVALLAVIYLNQVVRGQRVLCIL
 KEQISNEGEDKIFLNKLHSYERKERERSRVGTTEAAPALLTDEQDA"

BASE COUNT 333 a 555 c 558 g 358 t
ORIGIN

Alignment Scores:

Pred. No.: 6.27e-23 Length: 1804
Score: 293.00 Matches: 63
Percent Similarity: 53.76% Conservative: 37
Best Local Similarity: 33.87% Mismatches: 66
Query Match: 29.24% Indels: 20
DB: 9 Gaps: 3

US-09-895-298A-83 (1-190) x BC018346 (1-1804)

QY 1 MetMetAsnPhgInProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
Db 1022 CTGCCCAACTGCCAGCGCCGCCGCCCTGGCTGCCTCACACATGAGCACCGCTTTC 1081
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
Db 1082 CTCACGCTGCTGCTGCTTCCCGCCCTTCTGGCGCGCTGTCTTCTGCTACGCCGCTC 1141
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 1142 TGGCAGGTGAAGCCCTCGACACACCTTCTTCCGACCCCTGGACACCATGTACGAG 1201
QY 61 SerIleTyrSerTrpIleAspThrLeu---SerThrArgProGlyTyrLeuTrpValVal 79
Db 1202 GCCGCGAGGCTGTGGGTGGGCCACCTGGAGCGCGGACGCCCGCTCTGCTGCCCTGCC 1261
QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleVal 99
Db 1262 TGGGTGCACCCGTAACCTGTGAAACACCTTCTTGTCTTCTGTCGACGCCCTGCTG 1321
QY 100 LeuIleIleThrTyrLeuTyrTrpGlnIleThrGlyArgGlyLysIleMetIleArgLeu 119
Db 1322 CTGGCGGTGATCTACCTCAACATCCAGGTGCTGGCGGCCACGCCAAGGTATCTGCCCTG 1381
QY 120 LeuHisGlnGlnIleIleAsnGlnGlyLysAspLysMetPheLeuIleGlnLysLeuIle 139
Db 1382 CTCAGGAGCAGATGACATGAGGCTGAGGACAAAATCTTCTAATCAACAAGCTTCAC 1441
QY 140 LysLeuGlnAsp-----MetGlnLysLys 147
Db 1442 TCCATCTACGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1501
QY 148 AlaAsnProSerSerLeuValLeuGlnArgGlnValGlnGlnGlnGlnPheLeuHis 167
Db 1502 GCGGCACCCCTGCTGCTCAGACATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1540
QY 168 LeuGlyGlnHisAspGly 173
Db 1541 TAGGGGACGCGGATGGG 1558

RESULT 14
AK074065

LOCUS AK074065 5291 bp mRNA linear PRI 15-FEB-2002
DEFINITION Homo sapiens mRNA for FLJ00136 protein.
ACCESSION AK074065
VERSION AK074065.1 GI:18676477
KEYWORDS fls (full insert sequence).
SOURCE Homo sapiens adult spleen cDNA to mRNA, clone:FLJ00136.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
TITLE The nucleotide sequence of a long cDNA clone isolated from human spleen

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AUTHORS Jikuya,H., Takano,J., Nomura,N., Kikuno,R., Nagase,T. and Ohara,O.
TITLE Direct Submission

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COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert and 5'-8 3'-end one pass sequencing; Research Association for Biotechnology; cDNA library construction and clone selection; Kazusa DNA Research Institute.

FEATURES

source location/Qualifiers
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/dev_stage="adult"
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/evidence=not_experimental
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LHSLGLALISALQALMPWRALKRIGQFGSSVLYFLKTLIAFNALLLLVAFI
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PSTSGPRFLDTMYEAGRVWVRLHLAGRPVSLPWRVRYLMENTFVFLVSALLLA
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AAPALLTDEQDA"

BASE COUNT 915 a 1642 c 1700 g 1034 t
ORIGIN

Alignment Scores:
Pred. No.: 2.45e-22 Length: 5291
Score: 293.00 Matches: 63
Percent Similarity: 53.76% Conservative: 37
Best Local Similarity: 33.87% Mismatches: 66
Query Match: 29.24% Indels: 20
DB: 9 Gaps: 3

US-09-895-298A-83 (1-190) x AK074065 (1-5291)

QY 1 MetMetAsnPhgInProProSerLysAlaTrpArgAlaSerGlnMetThrPhe 20
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QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40
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QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
Db 2177 TGGCAGGTGAAGCCCTCGACACACCTTCCGCGCGCTGTGAGACACCATGTACGAG 2236
QY 61 SerIleTyrSerTrpIleAspThrLeu---SerThrArgProGlyTyrLeuTrpValVal 79
Db 2237 GCCGCGAGGCTGTGGGTGGGCCACCTGGAGCGCGGACGCCCGCTGCTGCTGCCCTGCC 2296
QY 80 TrpIleTyrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuIleVal 99

